

In the Claims

Please replace all prior versions, and listings, of claims in the application with the following list of claims:

1-35. (Canceled)

36. (Currently Amended) A method for determining whether monosaccharides or disaccharides of a query sequence match monosaccharides or disaccharides of a polysaccharide, wherein the query sequence is represented by a first data structure, tangibly embodied in a computer-readable medium, including an identifier that includes one or more fields, each field for storing a value for the monosaccharides or disaccharides of the query sequence, and wherein the polysaccharide is not a nucleic acid and is represented by a second data structure, tangibly embodied in a computer-readable medium, including an identifier that includes one or more fields, each field for storing a value for the monosaccharides or disaccharides of the polysaccharide, wherein one or more of the values of the second data structure correspond to the nature and degree of sulfation or acetylation of the monosaccharide or disaccharide of the polysaccharide ~~wherein the identifier includes a value for a disaccharide of the polysaccharide,~~ the method comprising acts of:

(A) a user providing input for the one or more fields of the first data structure with an input device;

(B) generating at least one mask with the values stored in the one or more fields of the first data structure;

(C) performing at least one binary operation on the values stored in the one or more fields of the second data structure using the at least one mask to generate at least one result; and

(D) determining whether the monosaccharides or disaccharides of the query sequence match the monosaccharides or disaccharides of the polysaccharide with the at least one result.

37. (Original) The method of claim 36, wherein each of the one or more fields of the first and second data structures is a bit field.

38-53. (Canceled)

54. (Previously Presented) The method of claim 36, wherein each of the one or more fields of the first and second data structures is a non-character based field.

55. (Previously Presented) The method of claim 36, wherein each of the identifiers of the first and second data structures is represented as a numerical identifier.

56. (Previously Presented) The method of claim 55, wherein each of the identifiers of the first and second data structures is represented as a single digit hexadecimal number.

57. (Previously Presented) The method of claim 55, wherein each of the identifiers of the first and second data structures is represented as a decimal value.

58. (Previously Presented) The method of claim 57, wherein the decimal value may be reduced to a plurality of prime divisors.

59. (Previously Presented) The method of claim 36, wherein the monosaccharide or disaccharide of the polysaccharide is a monosaccharide.

60. (Previously Presented) The method of claim 36, wherein the monosaccharide or disaccharide of the polysaccharide is a disaccharide.

61. (Previously Presented) The method of claim 36, wherein the value corresponding to the monosaccharide or disaccharide of the polysaccharide corresponds to one or more properties of the monosaccharide or disaccharide of the polysaccharide.

62. (Previously Presented) The method of claim 61, wherein the one or more properties comprises the identity of the monosaccharide or disaccharide of the polysaccharide.

63. (Previously Presented) The method of claim 61, wherein the one or more properties comprises the exact chemical structure as defined by the basic building block of the polysaccharide.

64. (Previously Presented) The method of claim 61, wherein the one or more properties comprises the charge of the monosaccharide or disaccharide of the polysaccharide.

65. (Previously Presented) The method of claim 61, wherein the one or more properties comprises the molecular weight of the monosaccharide or disaccharide of the polysaccharide.

66. (Previously Presented) The method of claim 61, wherein the one or more properties comprises the nature and degree of sulfation of the monosaccharide or disaccharide of the polysaccharide.

67. (Previously Presented) The method of claim 61, wherein the one or more properties comprises the nature and degree of acetylation of the monosaccharide or disaccharide of the polysaccharide.

68. (Previously Presented) The method of claim 61, wherein the one or more properties comprises the nature or identity of substituents of the monosaccharide or disaccharide of the polysaccharide.

69. (Previously Presented) The method of claim 61, wherein the act of determining includes an act of determining that one or more properties of the monosaccharide or disaccharide of the query sequence match the one or more properties of the monosaccharide or disaccharide of the polysaccharide when the at least one result has a non-zero value.

70. (Previously Presented) The method of claim 36, wherein the monosaccharide or disaccharide of the polysaccharide is a monosaccharide or disaccharide of a heparin-like glycosaminoglycan.

71. (Previously Presented) The method of claim 36, wherein the at least one binary operation includes at least one logical AND operation.

72. (Previously Presented) The method of claim 37, wherein the at least one binary operation includes acts of performing a logical AND operation on the values stored in the one or more bit fields of the second data structure using each of the at least one mask to generate intermediate results, and combining the intermediate results using at least one logical OR operation to generate the at least one result.

73. (Currently Amended) A method for determining whether a disaccharide of a query sequence matches a disaccharide of a heparin-like glycosaminoglycanpolysaccharide, wherein the query sequence is represented by a first data structure, tangibly embodied in a computer-readable medium, including an identifier that includes one or more fields, each field for storing a value for the query sequence, and wherein the heparin-like glycosaminoglycanpolysaccharide ~~is not a nucleic acid~~ and is represented by a second data structure, tangibly embodied in a computer-readable medium, including an identifier that includes one or more fields, each field for storing a value for the heparin-like glycosaminoglycanpolysaccharide, the method comprising acts of:

(A) a user providing input for the one or more fields of the first data structure with an input device;

(B) generating at least one mask with the values stored in the one or more fields of the first data structure;

(C) performing at least one binary operation on the values stored in the one or more fields of the second data structure using the at least one mask to generate at least one result; and

(D) determining whether the disaccharide of the query sequence match the disaccharide of the heparin-like glycosaminoglycan~~polysaccharide~~ with the at least one result.

74. (New) The method of claim 61, wherein the one or more properties comprises the presence or absence of C5 epimerization of the monosaccharide or disaccharide of the polysaccharide.

75. (New) The method of claim 73, wherein one or more of the values of the second data structure correspond to the nature and degree of sulfation or acetylation of the disaccharide of the heparin-like glycosaminoglycan.

76. (New) The method of claim 73, wherein one or more of the values of the second data structure correspond to the presence or absence of C5 epimerization.

77. (New) The method of claim 75, wherein one or more of the values of the second data structure correspond to the presence or absence of C5 epimerization.